



GeneInfo version 4.5
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EM protein - protein search, using SW model

Run on: February 20, 2002, 16:27:32 : Search time 17.06 seconds

(without alignments)
898 354 Million cell updates/sec

Title: US-09-534-376a-13

Sequence: 1 MRLHMLSLQVTLAAQAVL.....LAAHVCGRVSRKRLHM 418

Scoring table:
BLAST/BLAST
Gapop 10.0, Gapext 0.5

Searchset: 100059 seqs, 36664627 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post processing: Minimum Match 0%

Maximum Match 100%

Database: 1 SWISSPROT_39.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length for	ID	Description
1	1604.5	76.7	419	VEGF_HUMAN
2	1747.5	74.2	415	VEGF_MOUSE
3	241	10.2	1700	BAR1_CHITE
4	199	8.5	235	VEGF_HUMAN
5	191.5	8.1	190	VEGF_PIC
6	188.5	8.0	164	VEGF_RAT
7	179.5	7.6	164	VEGF_CAVO
8	174.5	7.4	190	VEGF_BOVIN
9	174.5	7.4	214	VEGF_MOUSE
10	169	7.2	214	VEGF_CHICK
11	164.5	7.0	188	VEGF_MOUSE
12	162.5	6.9	188	VEGF_HUMAN
13	158.5	6.7	145	VEGF_SHEEP
14	152	6.5	2871	VEGF_MOUSE
15	150	6.4	148	VEGF_GREN7
16	147.5	6.3	170	PLGF_HUMAN
17	147	6.2	2871	VEGF_HUMAN
18	146.5	6.2	134	VEGF_PIC
19	144	6.1	2871	VEGF_MOUSE
20	141.5	6.0	1712	VEGF_HUMAN
21	141	6.0	380	VEGF_MOUSE
22	140	5.9	2871	VEGF_MOUSE
23	138	5.9	812	VEGF_RAT
24	137.5	5.8	1104	VEGF_HUMAN
25	137.5	5.8	1964	VEGF_MOUSE
26	136.5	5.8	473	VEGF_MOUSE
27	136.5	5.8	1808	VEGF_MOUSE
28	135	5.7	2318	VEGF_MOUSE
29	134.5	5.7	2201	VEGF_HUMAN
30	134	5.7	2704	VEGF_MOUSE
31	134.5	5.7	810	VEGF_RAT
32	132.5	5.6	810	VEGF_HUMAN
33	132	5.6	810	VEGF_HUMAN

34	132	5.6	2813	VEGF_CAVO	Q28295 canis fami
35	131.5	5.6	2531	VEGF_MOUSE	Q01705 mus muscu
36	131	5.6	158	VEGF_MOUSE	P49764 mus muscu
37	129.5	5.5	1106	VEGF_MOUSE	P40798 drosophila
38	129.5	5.5	1408	VEGF_MOUSE	P18168 drosophila
39	128	5.4	2813	VEGF_HUMAN	P04275 homo sapien
40	128	5.4	3051	VEGF_CAVO	P44576 canis fami
41	128	5.4	5376	VEGF_MOUSE	C88759 mus muscu
42	127	5.4	1429	VEGF_MOUSE	P14585 canis fami
43	126.5	5.4	241	VEGF_MOUSE	C04226 ovine arthr
44	126.5	5.4	1877	VEGF_MOUSE	Q04592 mus muscu
45	126	5.4	575	VEGF_HUMAN	P07204 homo sapien

ALIGNMENTS

RESULT: 1
VEGF_HUMAN
ID VEGF_HUMAN STANDARD PKI 419 AA
AC P49767
DT 01-OCT-1996 (Ref. 34, last sequence update)
DT 01-OCT-1996 (Ref. 34, last sequence update)
FT 20-AUG-2001 (Ref. 40, last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (VASCULAR
ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRF) (F114 LIIGAND) (F114-
L).
GN VEGFC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eularchia; Primates; Catarrhini; Hominoidea; Homo.
CX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 103-120.
RX MEDLINE:96178224; PubMed:8617204;
RA Tokov V., Pajusola K., Kallipon A., Chillov P., Laitinen I., Kork E.,
RA Saksela O., Kallipon N., Allitalo K.,
RT "A novel vascular endothelial growth factor, VEGF-C, is a ligand for
the Flt4 (VEGFR-3) and Klf2 (VEGFR-2) receptor tyrosine kinases".
RL EMBO J. 15:290-298(1996).
RN [2]
RP EPRAFUM.
RX MEDLINE:96203094; PubMed:8612600;
RA Sokob V., Pajusola K., Sarpinen A., Chillov P., Laitinen I., Kork E.,
RA Saksela O., Kallipon N., Allitalo K.,
RL EMBO J. 15:1751-1761(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE:96319526; PubMed:870972;
RA Lee J., Garg A., Yoon J., Jacob S.M., Avraham H., Wood W.L.,
RT "Vascular endothelial growth factor-related protein a ligand and
specific activator of the tyrosine kinase receptor Flt4".
RL Proc. Natl. Acad. Sci. U.S.A. 93:1988-1992(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA Fitz L., Morris J.C., Towler P.S., Long A.J., Greco R.,
RA Burgess P., Giannelli J., Charleita A., Hennessy D., Kozaric S.,
RA Fitzpatrick M., Scully B., Welch R., Nelson S., Finnerty H.,
RA Zoller R., Wang J., Nickbarg E., Gassaway R., Turner K.,
RA Wood C.R.,
RT "Soluble Flt4 (Flt4-ecto) is the EMG/Receptor/ligand databases.
CC -1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CELL GROWTH.
CC -1- SOURCE: BOMBIKIN; DISULFIDE-LINKED.
CC -1- TIME: PROBABLY PROTEOLYTICALLY PROCESSED IN THE C-TERMINUS.
CC -1- SIMILARITY: RELATED TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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EMBL: X94415; CAA6707.1;
EMBL: 044142; AAB6214.1;
EMBL: 058111; AAB6707.1;
EMBL: F15692; TYPE;
MIM: 601528;
InterPro: IP000400; CF_CYSKNOT;
InterPro: IP00072; P66P;
Pfam: PF00441; P66P.1;
Pfam: PF00498; GPCYSKNOT;
ProDom: P0001629; P66P.1;
SMART: SM00141; P66P.1;
PROSITE: PS00249; P66P_1; 1;
PROSITE: PS0278; P66P_2; 1;
Molecule: Growth factor; Glycoprotein; Signal; Repeat.
ET STOMAL. 1
ET PROPEP. 2 102 POTENTIAL.
ET CHAIN. 103 419 VASCULAR ENDOTHELIAL GROWTH FACTOR C.
ET DOMAIN. 275 465 4 X 24 AA TANDEM REPEATS.
ET REPEAT. 275 298 1.
ET REPEAT. 299 322 2.
ET REPEAT. 323 346 4.
ET REPEAT. 347 365 4 (PARTIAL).
ET CARBOHYD. 175 175 N-LINKED (GLYNA). (POTENTIAL).
ET CARBOHYD. 205 205 N-LINKED (GLYNA). (POTENTIAL).
ET CARBOHYD. 240 240 N-LINKED (GLYNA). (POTENTIAL).
SEQUENCE 419 AA; 4688 MW; 99598719084014E CRC64.

Query Match 76.7%; Score 1804.5; D0 1; Length 419;
Host Local Similarity 76.7%; Pred. No. 5; No-130;
Matches 419; Conservative 47; Mismatches 60; Indels 3; Gaps 3.

1 MLLLESLSTGLAAGAVILGPGQ-PIVAAAYESHHYEEHPVAGDEKAKASHDEEOL 59
1 MLLLESLSTGLAAGAVILGPGQ-PIVAAAYESHHYEEHPVAGDEKAKASHDEEOL 59
1 MLLLESLSTGLAAGAVILGPGQ-PIVAAAYESHHYEEHPVAGDEKAKASHDEEOL 59
60 RSVSVDELMLVLYEYKMKR-KVQPKAWQNHSSSSTESDSLEAAAHYALILK 119
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Query Match 74.2%; Score 1747.5; D0 1; Length 415;
Host Local Similarity 74.0%; Pred. No. 5; No-130;
Matches 415; Conservative 47; Mismatches 65; Indels 7; Gaps 4.

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100 RSVSVDELMLVLYEYKMKR-KVQPKAWQNHSSSSTESDSLEAAAHYALILK 119


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VEGF_P13
ID VEGF_P13 STANDARD: PRT: 190 AA.
DI 01-FEB-1996 (rel. 33, created)
DI 01-FEB-1996 (rel. 33, last sequence update)
DI 20-AUG-2001 (rel. 40, last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE PERMEABILITY FACTOR) (VPF).
GN VEGF.
OS Sus scrofa (Pig);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID:9623.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:95143284; PubMed 7841203;
FA Shattil H.S., Tani T.H., Cho H.C.H., Verdow P.V.;
RT "Nucleotide sequence and expression of the porcine vascular
RT endothelial growth factor."
RT Biochim. Biophys. Acta 1260:235-238(1995).
CC -1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC PERMEABILITY (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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CC or send an email to license@ebi.ac.uk).
CC
CC FMBL: X61380; CAA57143.1;
CC HSSP: P15692; 2VGH.
CC InterPro: IPR000072; PDGF.
CC Pfam: PF00441; PDGF_1.
CC ProDom: PD001629; PDGF_1.
CC SMART: SM00141; PDGF_1.
CC PROSITE: PS00249; PDGF_1;
CC PROSITE: PS00278; PDGF_2;
CC KW Mitogen; Growth factor; Glycoprotein; Signal.
CC FT SIGNAL 1 26
CC FT CHAIN 27 190 VASCULAR ENDOTHELIAL GROWTH FACTOR.
CC FT DISULFID 51 93 BY SIMILARITY.
CC FT DISULFID 92 127 BY SIMILARITY.
CC FT DISULFID 85 129 BY SIMILARITY.
CC FT DISULFID 76 74 INTERCHAIN (BY SIMILARITY).
CC FT DISULFID 85 85 INTERCHAIN (BY SIMILARITY).
CC FT CARBOHYD 100 100 N-LINKED GLYCANA... (POTENTIAL).
CC SEQUENCE 190 AA: 22468 MW: 94140879.10477 CIRC64;
Query Match 8.1%; Score 191.5; DB 1; Length 190;
Best Local Similarity 27.5%; Pred. No. 2,6e-08;
Matches 49; Conservative 39; Mismatches 68; Indels 31; Gaps 6;
DB 116 ELKSTFFRKQMPDEWVWVQKPPATNTFFKPPVSVVPGGCGSESLQGMNI 176
111 11 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 38 EVKREMLV YKSYCKRPFELVLFQFRTDGLHITKNSCYGLKRCGQNDDEGLDQ-V 94
111 11 111 111 111 111 111 111 111 111 111 111 111 111
DB 176 STNYSTLFTTVPISHPKIVSSTANHSCHMSLWYQVYSILPESLFAIQVQ 295
111 11 111 111 111 111 111 111 111 111 111 111 111 111
DB 95 PTEHNILMLMHLKTHQGLHGMSTLQGNCTGCKNVAQV-----ENQ 142
111 11 111 111 111 111 111 111 111 111 111 111 111 111
DB 430 IYANKTCKKAWNNLITGVAHPTGSHSTGSGGSGTGVVQVNGFSTGCTG 292
111 11 111 111 111 111 111 111 111 111 111 111 111 111
DB 143 GDSERRKH EVDGPTGTRK-----NLS-----KAWGTE NPTLTD 185
111 11 111 111 111 111 111 111 111 111 111 111 111 111

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RESULT 6
VEGF_RAT
ID VEGF_RAT STANDARD: PRT: 190 AA.
DI 01-AUG-1990 (rel. 15, created)
DI 01-AUG-1990 (rel. 15, last sequence update)
DI 20-AUG-2001 (rel. 40, last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
DE PERMEABILITY FACTOR) (VPF).
GN VEGF.
OS Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muridae; Rattus.
OX NCBI_TaxID:10116;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 27-190.
RX MEDLINE:96207219; PubMed 220579;
FA Conn G., Rayne M.L., Soderman D.D., Kwok P.W., Sullivan K.A.,
FA Palasi T.M., Bopp D.A., Thomas K.A.;
RT "Amino acid and cDNA sequences of a vascular endothelial cell mitogen
RT that is homologous to platelet-derived growth factor."
RL Proc. Natl. Acad. Sci. U.S.A. 87:2628-2633(1990).
CC -1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
CC CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
CC PERMEABILITY.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
CC TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
CC SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE PITUITARY, IN BRAIN, IN
CC PARTICULARLY IN SUPRACORTIC AND PARAVENTRICULAR NUCLEI AND THE
CC CHOROID PLEXUS. ALSO FOUND ABUNDANTLY IN THE CORPUS LUTEUM OF
CC THE OVARY AND IN KIDNEY GLOMERULI.
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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CC or send an email to license@ebi.ac.uk).
CC
CC FMBL: M32167; AAA42111.1;
CC PIR: A35987; A35987.
CC HSSP: P15692; 2VGH.
CC InterPro: IPR000072; PDGF.
CC Pfam: PF00441; PDGF_1.
CC ProDom: PD001629; PDGF_1.
CC SMART: SM00141; PDGF_1.
CC PROSITE: PS00249; PDGF_1;
CC PROSITE: PS00278; PDGF_2;
CC KW Mitogen; Growth factor; Glycoprotein; Signal.
CC FT SIGNAL 1 26
CC FT CHAIN 27 190 VASCULAR ENDOTHELIAL GROWTH FACTOR.
CC FT DISULFID 51 93 BY SIMILARITY.
CC FT DISULFID 82 127 BY SIMILARITY.
CC FT DISULFID 86 129 BY SIMILARITY.
CC FT DISULFID 76 74 INTERCHAIN (BY SIMILARITY).
CC FT DISULFID 85 85 INTERCHAIN (BY SIMILARITY).
CC FT CARBOHYD 100 100 N-LINKED GLYCANA... (POTENTIAL).
CC SEQUENCE 190 AA: 22496 MW: 58937401041977 CIRC64;
Query Match 8.0%; Score 188.5; DB 1; Length 190;
Best Local Similarity 22.1%; Pred. No. 4.5e-08;
Matches 57; Conservative 44; Mismatches 68; Indels 99; Gaps 10;
DB 41 IHLKSSSTKSNSTLFTTVPISHPKIVSSTANHSCHMSLWYQVYSILPESLFAIQVQ 170
111 11 111 111 111 111 111 111 111 111 111 111 111 111
DB 19 EVKREMLV YKSYCKRPFELVLFQFRTDGLHITKNSCYGLKRCGQNDDEGLDQ-V 94
111 11 111 111 111 111 111 111 111 111 111 111 111 111

```


RESULT 14
 VEGF_SHEEP STANDARD: PRT: 146 AA.
 AC P50412;
 DE 01-OCT-1996 (Ref. 44, created)
 DE 01-OCT-1996 (Ref. 44, last sequence update)
 DE 20-AUG-2001 (Ref. 40, last annotation update)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR
 PERMEABILITY FACTOR) (VPF).
 VEGF.
 OS ovine (sheep).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Caprinae; Ovis.
 CC NCBI TaxId=9940;
 RN 111
 RP SEQUENCE FROM N.A.
 RX TISSUE-Kidney;
 RX MEDLINE=97117958; PubMed=8958842;
 RA Reddy D.A., Dai Y., Li J., Charnock-Jones D.S., Smith S.K.,
 RA Reynolds L.P., Moor R.M.;
 RT Characterization and expression of vascular endothelial growth
 RT factor (VEGF) in the ovine corpus luteum.
 RL J. Reprod. Fert. 11, 108:157-165(1996).
 CC 1 FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL
 CC CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR
 CC PERMEABILITY.
 CC 1 SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC 1 SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
 CC TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY
 CC SIMILARITY).
 CC 1 SIMILARITY: BELONGS TO THE VEGF/FAMILY OF GROWTH FACTORS.
 CC
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100 94 VEGF_MOUSE
 RESULT 14
 PBNL_MOUSE STANDARD: PRT: 2871 AA.
 AC Q61554; Q60826;
 DE 01-NOV-1997 (Ref. 45, created)
 DE 01-NOV-1997 (Ref. 45, last sequence update)
 DE 01-NOV-1997 (Ref. 45, last annotation update)
 DE FIBRILIN-1 PRECURSOR.
 DE FBN1 or FBN 1.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI TaxId=10090;
 RN 111
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95140561; PubMed 7829516;
 RA Yin W., Gormley J., Sanguinetti C., Smiley E., Partridge T.,
 RA Pereira L., Ramirez F., Bonadio J.;
 RT Primary structure and developmental expression of Fbn-1, the mouse
 RT fibrillin gene.
 RL J. Biol. Chem. 270:1798-1806(1995).
 RN 121
 RP SEQUENCE FROM N.A.
 RP STRAIN CD-1; TISSUE Kidney;
 RA Cha K., Kumar A., Wada J., Liu Z., Kanwar Y.S.;
 RA Submitted (APR-1995) to the EMBL/Genbank/DDBJ databases.
 CC 1 FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
 CC THAT BINS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE
 CC LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
 CC 1 FIBRILLIN-1 MOLECULES OR WITH OTHER COMPONENTS OF THE
 CC MICROFIBRILS (BY SIMILARITY).
 CC 1 SIMILARITY: CONTAINS 43 CALCIUM BINDING AND 4 NON-CALCIUM BINDING
 CC FOLD-LIKE DOMAINS.
 CC 1 SIMILARITY: CONTAINS 7 TCP-BETA BINDING PROTEIN DOMAINS.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation.
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ET	D MAIN	402	446	PRO-RICH
ET	D MAIN	449	489	PRO-LIKE 6, NON-CALCIUM BINDING
ET	D MAIN	490	529	EOF-LIKE 7, CALCIUM BINDING
ET	D MAIN	530	571	EOF-LIKE 7, CALCIUM BINDING
ET	D MAIN	572	612	EOF-LIKE 8, CALCIUM BINDING
ET	D MAIN	613	653	EOF-LIKE 9, CALCIUM BINDING
ET	D MAIN	654	693	EOF-LIKE 10, CALCIUM BINDING
ET	D MAIN	694	734	TORBP 2
ET	D MAIN	735	764	EOF-LIKE 11, CALCIUM BINDING
ET	D MAIN	765	806	EOF-LIKE 12, CALCIUM BINDING
ET	D MAIN	807	846	EOF-LIKE 13, CALCIUM BINDING
ET	D MAIN	847	886	EOF-LIKE 14, CALCIUM BINDING
ET	D MAIN	887	921	TORBP 3
ET	D MAIN	922	1018	EOF-LIKE 15, CALCIUM BINDING
ET	D MAIN	1019	1028	EOF-LIKE 16, CALCIUM BINDING
ET	D MAIN	1029	1112	EOF-LIKE 17, CALCIUM BINDING
ET	D MAIN	1113	1154	EOF-LIKE 18, CALCIUM BINDING
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ET	D MAIN	1197	1237	EOF-LIKE 20, CALCIUM BINDING
ET	D MAIN	1238	1279	EOF-LIKE 21, CALCIUM BINDING
ET	D MAIN	1280	1321	EOF-LIKE 22, CALCIUM BINDING
ET	D MAIN	1322	1362	EOF-LIKE 23, CALCIUM BINDING
ET	D MAIN	1363	1403	EOF-LIKE 24, CALCIUM BINDING
ET	D MAIN	1404	1445	EOF-LIKE 25, CALCIUM BINDING
ET	D MAIN	1446	1485	EOF-LIKE 26, CALCIUM BINDING
ET	D MAIN	1487	1527	TORBP 4
ET	D MAIN	1528	1599	EOF-LIKE 27, CALCIUM BINDING
ET	D MAIN	1600	1647	EOF-LIKE 28, CALCIUM BINDING
ET	D MAIN	1648	1688	TORBP 5
ET	D MAIN	1689	1758	EOF-LIKE 29, CALCIUM BINDING
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ET	D MAIN	1808	1848	EOF-LIKE 31, CALCIUM BINDING
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ET	D MAIN	1891	1929	EOF-LIKE 33, CALCIUM BINDING
ET	D MAIN	1930	1972	EOF-LIKE 34, CALCIUM BINDING
ET	D MAIN	1973	2014	EOF-LIKE 35, CALCIUM BINDING
ET	D MAIN	2013	2054	TORBP 6
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ET	D MAIN	2206	2246	EOF-LIKE 39, CALCIUM BINDING
ET	D MAIN	2247	2290	EOF-LIKE 40, CALCIUM BINDING
ET	D MAIN	2291	2331	TORBP 7
ET	D MAIN	2332	2400	EOF-LIKE 41, CALCIUM BINDING
ET	D MAIN	2401	2443	EOF-LIKE 42, CALCIUM BINDING
ET	D MAIN	2444	2484	EOF-LIKE 43, CALCIUM BINDING
ET	D MAIN	2485	2523	EOF-LIKE 44, CALCIUM BINDING
ET	D MAIN	2524	2566	EOF-LIKE 45, CALCIUM BINDING
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ET	D MAIN	2607	2647	EOF-LIKE 47, CALCIUM BINDING
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ET	D MAIN	2688	2727	BY SIMILARITY
ET	D MAIN	2728	2767	BY SIMILARITY
ET	D MAIN	2768	2807	BY SIMILARITY
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ET	D MAIN	3328	3367	BY SIMILARITY
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ET	D MAIN	3408	3447	BY SIMILARITY
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ET	D MAIN	4568	4607	BY SIMILARITY
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ET	D MAIN	5008	5047	BY SIMILARITY
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ET	D MAIN	5728	5767	BY SIMILARITY

[illegible]

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Page 13



SEQUENCE FROM N.A.
 EC LUSIP-SALIVARY GLAND
 RA Gusev S I, Gusev G, Holt W C, Hoffman E T, Martin J, Hamilton R J
 BL Submitted (Apr-1996) to the EMBL/GenBank/TrEMBL databases.
 DR EMBL: H54641; AAA94904.1;
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR000561; Multithionin domain.
 DR PRINTS: PR00076; MTNEMAD00F.
 DR PROSITE: PS00022; EGF_1; EGF_2; EGF_3;
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 SQ SEQUENCE: 1794 AA; 185245 MW; 3482621734128 CYS11.

Query Match 9.98; Score 231; DB 5; Length 1704;
 Best local similarity 19.78; Pred. No. 1.6e-13;
 Matches 90; Conservative 52; Mismatches 192; Indels 122; Gaps 17;

QY EEERAPAPRAHASKIFELPSSVSDPIMIVPPYWMKQLEPKQWJHPEHSS 98
 DB DEMONSTRAPAWSHITPRKKAHAFATVA---EYMLNCE---KQYLAASKOMTA 1016
 QY 49 ITRSDISIKFAAHYNAFIIKSTIPWPKTQQ-----MREPVVDLCK--- 141
 DB 1017 ENKREDAATSCVGRSP--MNSVLEGRKWNNECALERANVGNKAPQRMIDNICKTC 1074
 QY 142 -----EGGATNTFFKPPVSYR-----GGGQNSHGIGQMNISTN 178
 DB 1075 PUVNINPAKGTIFHSETPQCT---KRECLDPFNSIPEQVVDLCKQCGKQLEPK 1130
 QY 179 YISKLEETIVP-----LSHGRKPVTV---VSFANHISCKQMSKLDVY 217
 DB 1141 NICKGKPPNKPVSQKQKTKTPVPSCKKSPKAPNAPQVQENKPPKPPKPS 1190
 QY 218 KQV-----HETRESLALGICHVAN-----KCTKHHYWNQI 252
 DB 1191 KTFPRGKNNWQVQCTPAFVSASQVSNVTSQVNWMPVQVQVNWVNS 1250
 QY 253 GPTAAGHDPESHGDSITSEPHIGPFELEELQGVKGVPEISQIKELDPA 312
 DB 1251 GVVV-----PKNPKRANQ--NKKMNKACETPRKPPGPPVAGVQVAKWNN 1298
 QY 313 SQGQMG-KNKIIPSSQPNKFFEPKQGVVYKT-----QPKHPI NPAKQTEETSPN 366
 DB 1299 TGAECPPGKALFASQDQKSWQDSQVCKSKMPGQTPNQCWQNEETQCF--SGT 1356
 QY 367 KPIKRRKHHPHGGCYPRPTVYTKKQAGLILAFVQGV 408
 DB 1357 QTPVAGSWISQTCQSCP-----ATKCTTAQFWAKQKQV 1394

RESULT 9
 ID Q9H1W9 PRELIMINARY; PRT: 232 AA.
 AC Q9H1W9;
 DT 01-MAR-2001 (TEMBLrel. 16, created)
 DT 01-MAR-2001 (TEMBLrel. 16, last sequence update)
 DT 01-JUN-2001 (TEMBLrel. 17, last annotation update)
 DE D1261522.6.3 (VASCULAR ENDOTHELIAL GROWTH FACTOR).
 GN VEGF.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX Nsl_taxonomy 9609;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Williams S.
 BL Submitted (Dec-2000) to the EMBL/GenBank/TrEMBL databases.
 DR EMBL: AL16161; CAC19612.1;
 DR InterPro: IPR000072; PDGF.
 DR Pfam: PF00441; PDGF_1.
 DR Pfam: PF001629; PDGF_1.
 DR SMART: SM00441; PDGF_1.
 DR PROSITE: PS00249; PDGF_1; 1.

DR PROSITE: PS00278; PDGF_2; 1.
 SQ SEQUENCE: 232 AA; 27042 MW; 58495644464D01 CYS64.

Query Match 9.98; Score 211.5; DB 4; Length 254;
 Best local similarity 24.28; Pred. No. 1.4e-12;
 Matches 68; Conservative 43; Mismatches 105; Indels 75; Gaps 10;

QY 68 LMAVAVVWRKQVQLERQDGMKNSLSQTEFSTQRIAAADYNAELTSLTMMR 127
 DB 14 LLYVIAVWQAVMAVQDQNNH-----LVVEFMIV-YGR 49
 QY 128 TQSMREPVVGLSKPATNTFFKPPVSYRQVSDGQNSQGLQMNISTNTSTLTFI 187
 DB 50 SYCHPFLIVHFGVPPPTFTYTPKQSVQIMVQVQNNPFI PVVTPFNSIMLMKRI 109
 QY 188 TVPLSHGRKIVVVSFANHISCKQMSKLDVYVPSLALGICHVANQVKNV 247
 DB 110 K--HVVQHTQMSPTQJNNKTPPKRQVAPQKRSVQK---KQYLAASKOMTA 162
 QY 248 WNNQI-GPTAAGHDPESHGDSITSEPHIGQPKK-----LDEITGVVKNV 299
 DB 163 MSVVYCARQCLM-----PWSLPGHPPGQSEKHKHLPVQVDTCKQSK--- 207
 QY 300 PISGPIPKPTDPAQGVWFKNKIIPSSQPNKFFEPKQGV 340
 DB 208 -----NTDSCKAKQL-----ELNERTQ 227

RESULT 10
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 AC Q16889; PRELIMINARY; PRT: 254 AA.
 DT 01-NOV-1996 (TEMBLrel. 01, created)
 DT 01-NOV-1996 (TEMBLrel. 08, last sequence update)
 DT 02-JUN-2001 (TEMBLrel. 17, last annotation update)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF).
 GN VEGF 206.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX Nsl_taxonomy 9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:92168017; PubMed:1794841;
 RA Hock K.A., Ferrara N., Winer J., Cachianes G., Li H., Long D.W.;
 DT "The vascular endothelial growth factor family: Identification of a
 PT fourth molecular species and characterization of alternative splicing
 RT of RNA."
 FL Mol. Endocrinol. 5:1806-1814(1991).
 DR EMBL: S85192; AAC63102.1;
 DR EMBL: S85224; AAC63101.1;
 DR EMBL: S85199; AAC63101.1; JOINED.
 DR EMBL: S85201; AAC63101.1; JOINED.
 DR EMBL: S85219; AAC63101.1; JOINED.
 DR EMBL: S85222; AAC63101.1; JOINED.
 DR HSBST: F15692; VPEF.
 DR InterPro: IPR000072; PDGF.
 DR Pfam: PF00441; PDGF_1.
 DR Pfam: PF001629; PDGF_1.
 DR SMART: SM00441; PDGF_1.
 DR PROSITE: PS00249; PDGF_1; 1.
 DR PROSITE: PS00278; PDGF_2; 1.
 FI NTLER 1
 SQ SEQUENCE: 254 AA; 24461 MW; 06999097249PAB CYS64;

Query Match 9.98; Score 211.5; DB 4; Length 254;
 Best local similarity 24.28; Pred. No. 1.6e-12;
 Matches 68; Conservative 43; Mismatches 105; Indels 75; Gaps 10;
 QY 68 LMAVAVVWRKQVQLERQDGMKNSLSQTEFSTQRIAAADYNAELTSLTMMR 127
 DB 14 LLYVIAVWQAVMAVQDQNNH-----LVVEFMIV-YGR 49

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Index: 192, 193

GenCore version 4.5
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1M protein - protein search, using SW model

Run on: February 20, 2002, 16:25:45 ; Search time 42.36 seconds

(without alignments)
730,940 Million cell updates/sec

Title: US-09-534-376A-13

Protein Score: 2354

Sequence: 1 MHLLEPM SLRPPY AAQAVII

11AAQVPPVPTSWPPHLMN 418

Scoring Table:

MSM062
Gapop: 10.0 ; Gapext: 0.5

Scored: 522463 seqs, 7407320 positions

Total number of hits satisfying chosen parameters: 522463

Minimum E8 seq length: 0
Maximum E8 seq length: 20000000

Post-processing: Minimum Match: 08
Maximum Match: 1008

Listing first 45 summaries

Database:

A: Geneseq_1101:*

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- 2: /SILSR/qpdata/qgeneseq/qgeneseq/AA1981.DAT*
- 3: /SILSR/qpdata/qgeneseq/qgeneseq/AA1982.DAT*
- 4: /SILSR/qpdata/qgeneseq/qgeneseq/AA1983.DAT*
- 5: /SILSR/qpdata/qgeneseq/qgeneseq/AA1984.DAT*
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- 8: /SILSR/qpdata/qgeneseq/qgeneseq/AA1987.DAT*
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- 22: /SILSR/qpdata/qgeneseq/qgeneseq/AA2001.DAT*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2354	100.0	418	18	AAW00934
2	2354	100.0	418	19	AAW57543
3	1804.5	76.7	419	18	AAW17847
4	1804.5	76.7	419	18	AAW00932
5	1804.5	76.7	419	19	AAW57410
6	1804.5	76.7	419	20	AAW62013
7	1804.5	76.7	419	21	AAW10648
8	1804.5	76.7	419	21	AAW59048
9	1804.5	76.7	419	21	AAW70749
10	1804.5	76.7	419	21	AAW70962
11	1804.5	76.7	419	22	AAW17905

12	1795.5	76.3	419	18	AAW13833	Human vascular end
13	1794.5	76.2	419	20	AAV30518	Vascular endothel
14	1794.5	76.2	419	20	AAV22320	Full length human
15	1794.5	76.2	419	21	AAV97144	Vascular endothel
16	1794.5	76.2	419	22	AAV97570	Human VEGF-C prote
17	1793.5	76.2	419	19	AAW75751	Vascular endothel
18	1791.5	76.1	419	18	AAW11478	Human vascular end
19	1789.5	74.7	399	20	AAW62317	Human VEGF-C full
20	1747.5	74.2	415	19	AAW57542	Mouse VEGF-C and
21	1742.5	74.0	415	18	AAW00933	A truncated vascul
22	1603	68.1	350	28	AAV30519	Truncated human VE
23	1604	68.1	350	29	AAV72311	Truncated vascular
24	1604	68.1	350	21	AAV72315	Human VEGF-2 prote
25	1604	68.1	350	22	AAV72317	Human VEGF-2 prote
26	1599	67.9	350	16	AAW82486	Human VEGF-2 prote
27	1453	61.7	318	20	AAV08284	Human growth facto
28	1417	60.2	307	20	AAW86232	Human VEGF-C trunc
29	1391	59.1	302	20	AAW86233	Human VEGF-C trunc
30	1370	58.2	297	20	AAW86234	Human VEGF-C trunc
31	1343	57.1	292	20	AAW86235	Human VEGF-C trunc
32	677	28.8	325	19	AAW62240	Human VEGF-C trunc
33	677	28.8	325	22	AAV72320	Human VEGF-C trunc
34	677	28.8	325	19	AAW49036	Human VEGF-2 prote
35	677	28.8	354	19	AAW61341	Human VEGF-2 prote
36	677	28.8	354	19	AAW42493	Human VEGF-2 prote
37	677	28.8	354	21	AAW10649	Human VEGF-2 prote
38	677	28.8	354	21	AAW29049	Human VEGF-2 prote
39	677	28.8	354	21	AAV70750	Human VEGF-2 prote
40	677	28.8	354	21	AAV70983	Human VEGF-2 prote
41	677	28.8	354	22	AAV72573	Human VEGF-2 prote
42	677	28.8	354	22	AAW42606	Human VEGF-2 prote
43	677	28.8	354	22	AAW70965	Human VEGF-2 prote
44	667.5	28.4	347	20	AAV08286	Human growth facto
45	667.5	28.4	347	20	AAW61342	Human growth facto

ALIGNMENTS

RESULT 1	
AAW00934	Standard, Protein: 418 AA.
18	AAW00934
AC	AAW00934:
TT	13-NOV-1997 (11:57:00)
XX	
XX	Query: F114 receptor tyrosine kinase ligand VEGF-C
XX	
XX	VEGF-C, F114, receptor tyrosine kinase, VEGF-C, query:
XX	Vascular endothelial growth factor receptor-3, ligand:
XX	angiogenesis; wound healing; lymph vessels; therapy; diagnosis.
XX	
XX	Coturnix coturnix.
XX	
XX	13-FEB-1997.
XX	
XX	01-AUG-1996; 96W0-F100427.
XX	
XX	28-JUN-1996; 96US-0671573.
XX	01-AUG-1996; 96US-0510133.
XX	12-JAN-1996; 96US-0565805.
XX	14-FEB-1996; 96US-0601192.
XX	
XX	(UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX	
XX	Altado K. Joukov V.
XX	
XX	WPI, 1997 145688/13.
XX	
XX	N-PSDB; AAT84300.

Thu Feb 21 09:21:39 2002

us-09-534-376a-13.rag

Page 12

GenCorp version 4.5
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an M protein - protein search, using SW model

Run on:	February 20, 2002, 16:23:57 ; Search time 43.31 Seconds
	(without alignments)
	1401.594 Million cell updates/sec

Title:	US-09-534-376A-11
Portfolio:	2443

Sequencing:

1 MULLIGI,SLACSI,AAAI,IP, . . . ,SFSFEV,KQVPSYWRPHI,N 415

Scoring table: BLAST62
Gapop 10.0 , Gapext 0.5

47 rue des Rosiers, 14220 Eschdes

Total number of hits satisfying chosen parameters. 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post Processing: Minimum Match (8)

Indatubasi:

- 1: *SP_kirchhoff_17* *
- 2: *SP_bacteria* *
- 3: *SP_fungi* *
- 4: *SP_human* *
- 5: *SP_invertebrate* *
- 6: *SP_mammal* *
- 7: *SP_mice* *
- 8: *SP_orangeleaf* *
- 9: *SP_phase* *
- 10: *SP_plant* *
- 11: *SP_rodent* *
- 12: *SP_virus* *
- 13: *SP_veterbrate* *
- 14: *SP_unclassified* *

Print No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB	ID	Description
1	207.5	75.9	479	4	Q9XSC0	Q9XSC0 Bos taurus
2	176.2.5	75.5	418	4	Q57352	Q57352 Columba vicia
3	69.6	29.8	354	4	Q43415	Q43415 homo sapien
4	689.5	29.5	359	11	Q97946	Q97946 mus muscul
5	689	29.5	126	11	Q35757	Q35757 rattus norv
6	658.5	28.2	326	11	Q35251	Q35251 rattus norv
7	274.5	11.8	176	5	Q94446	Q94446 citellomys
8	260	11.1	159	5	Q94438	Q94438 citellomys
9	231	9.9	242	4	Q9H1W9	Q9H1W9 homo sapien
10	231	9.9	254	4	Q16889	Q16889 homo sapien
11	222.5	9.5	214	6	Q9MNV3	Q9MNV3
12	221.5	9.5	208	6	Q9XSP4	Q9XSP4 canis fami
13	217.5	9.3	209	4	Q60720	Q60720 homo sapien
14	217.5	9.3	214	6	Q9XSP5	Q9XSP5 canis fami
15	214.5	9.2	146	6	Q9XSF3	Q9XSF3 canis fami
16	212.5	9.1	140	6	Q9XSR0	Q9XSR0 equus caball
17	208.5	8.9	132	6	Q9CL52	Q9CL52 sus scrofa
18	205	8.8	122	6	Q9GLX1	Q9GLX1 bos taurus
19	203	8.7	144	4	Q9L752	Q9L752 xenopus lae

20	199.5	8.6	190	6	07764.4	07764.4	ovis aries
21	199.5	8.6	190	11	09087.9	09087.9	stax leon
22	199.5	8.6	191	4	07687.5	07687.5	homo sapien
23	196.5	8.4	214	11	09080.67	09080.7	rattus norv
24	195	8.4	174	4	0901.21	0911.21	homo sapien
25	190.5	8.2	190	11	09051.31	09051.3	mus mus
26	188.5	8.1	188	13	07466.2	07466.2	homo sapien
27	188.5	8.1	34	5	0901.81	0901.81	dirosophila
28	188.5	8.1	704	3	07456.7	07456.7	trichostema
29	187.5	8.0	171	4	090198	090198	homo sapien
30	184.5	7.9	147	4	090185	090185	homo sapien
31	184	7.9	142	11	09081.6	09081.6	mus mus
32	181.5	7.8	150	11	05488.1	05488.1	rattus norv
33	180	7.7	124	6	09080.0	09080.0	callithrix
34	180	7.7	301	5	09076.6	09076.6	dirosophila
35	177.5	7.7	148	13	04257.1	04257.1	xenopus lae
36	179.5	7.7	188	6	09854.8	09854.8	homo sapien
37	176.5	7.6	2352	5	06124.0	06124.0	homo sapien
38	176	7.5	326	6	09090.7	09090.7	macaca mula
39	176	7.5	800	5	09087.8	09087.8	dirosophila
40	172.5	7.4	18	6	09063.1	09063.1	ovis aries
41	172	7.4	247.1	4	06472.1	06472.1	homo sapien
42	172	7.4	247.1	4	0472.0	0472.0	homo sapien
43	171.5	7.4	170	11	090187	090187	rattus norv
44	170	7.3	247.1	11	09080.0	09080.0	rattus sp.
45	169.5	7.3	146	11	09080.6	09080.6	rattus norv

ALTERNATIVES

[illegible]

BL Submitted (0802-2000) to the EMBL Genbank/Genpep databases
 DR EMBL: AJ010418; CAA09179.1; -
 DR EMBL: AF062645; AAC16740.1; -
 DR EMBL: AL146141; CAC19514.1; -
 DR HSSP: P15692; 2VPE.
 DR InterPro: IPR000072; PDGF.
 DR Pfam: PF00841; PDGF_1.
 DR ProDom: PD001629; PDGF_1.
 DR SMART: SM00141; PDGF_1.
 DR PROSITE: PS00249; PDGF_1; 1.
 DR PROSITE: PS02784; PDGF_2; 1.
 DR Signal.
 DR Signal.
 ET CHAIN 1 26 POTENTIAL.
 ET SIGNAL.
 SV SEQUENCE 209 AA: 24422 MW: 24422 MW: FQICEACDQ45D6CA CQ664;

Query Match 9.48; Score 217.5; DB 6; Length 209;
 Best Local Similarity 26.48; Pred. No. H.1e-13;
 Matches 60; Conservative 27; Mismatches 75; Indels 67; Gaps 8;

QY 114 EITSTINWPKTQMPPEVTVVPPVATNTHTKPPVSVYPPNENSTAGMNT 172
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 DB 84 EVKPKK VVQSVVHPLHPLVQPEVPPPEVPPSGVPI MPQDQCNDELEVPI 97
 QY 174 STSTSKLITVITVQVSTVSTASGVSPPKTVVQVSTLQSTFALLVQ 172
 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 DB 98 EESNTIMIMIKINP-HVQGHIMSPHGLINKP-PKPKLQVQVSVQVQV 152
 QY 233 QANNTPTNVVWNNYMKCTAQDQPIFYSNVFHSINCHQVQPKKIDTHTQGVK 202
 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 DB 153 KKKKKSKP-----GQVSK----- 166

RESULT 14

QYXSF5 PRELIMINARY: PRT: 214 AA.

AC QYXSF5
 DT 01-NOV-1999 (EMBLrel. 12, created)
 DT 01-NOV-1999 (EMBLrel. 12, last sequence update)
 DT 01-JUN-2001 (EMBLrel. 17, last annotation update)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR 198
 GN VEGF.
 OS Carotis familiaris (dog).
 OC Eukaryota; Metazoa; Chordata; Graculata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID:9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE:HEART;
 RA Submitted by: Roque R.S.;
 RA Submitted (MAR 1993) to the EMBL/Genbank/Genpep databases
 DR EMBL: AF133250; AAC29684.1; -
 DR HSSP: P15692; 2VPE.
 DR InterPro: IPR000072; PDGF.
 DR Pfam: PF00841; PDGF_1.
 DR ProDom: PD001629; PDGF_1.
 DR SMART: SM00141; PDGF_1.
 DR PROSITE: PS00249; PDGF_1; 1.
 DR PROSITE: PS02784; PDGF_2; 1.
 SV SEQUENCE 214 AA: 24151 MW: 22666 MW: 22666 MW: 22666 MW: CQ664;

Query Match 9.48; Score 217.5; DB 6; Length 214;
 Best Local Similarity 26.48; Pred. No. H.1e-13;
 Matches 62; Conservative 26; Mismatches 75; Indels 79; Gaps 8;
 QY 109 HYNTEIKSTINWPKTQMPPEVTVVPPVATNTHTKPPVSVYPPNENSTAGMNT 168
 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 DB 84 EVKPKK VVQSVVHPLHPLVQPEVPPPEVPPSGVPI MPQDQCNDELEVPI 97
 QY 169 GNTSTYSLSTLFEITVPL SQPKVITSTFANHTSCGMSTLTVYRQVSHLR 223
 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 DB 93 CVPIEE-----FNITQIDIRKIPDQOHGKSTFQHSKTEGPKKIPAPQ----- 138
 QY 224 SLVATLQVQANAKICTNVVWNNYMKCTAQDQPIFYSNVFHSINCHQVQPKKIDTHTQGVK 202
 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 DB 153 KKKKKSKP-----GQVSK----- 166

14 64 EPHVAVVPM--VVQSVVHPLHPLVQPEVPPPEVPPSGVPI MPQDQCNDELEVPI 97
 QY 169 GNTSTYSLSTLFEITVPL-----SQPKVITSTFANHTSCGMSTLTVYRQVSHLR 223
 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 DB 93 CVPIEE-----FNITQIDIRKIPDQOHGKSTFQHSKTEGPKKIPAPQ----- 138
 QY 224 SLVATLQVQANAKICTNVVWNNYMKCTAQDQPIFYSNVFHSINCHQVQPKKIDTHTQGVK 202
 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 DB 153 KKKKKSKP-----GQVSK----- 166

Query Match 9.48; Score 217.5; DB 6; Length 209;
 Best Local Similarity 26.48; Pred. No. H.1e-13;
 Matches 60; Conservative 27; Mismatches 75; Indels 67; Gaps 8;

QY 114 EITSTINWPKTQMPPEVTVVPPVATNTHTKPPVSVYPPNENSTAGMNT 172
 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 DB 84 EVKPKK VVQSVVHPLHPLVQPEVPPPEVPPSGVPI MPQDQCNDELEVPI 97
 QY 174 STSTSKLITVITVQVSTVSTASGVSPPKTVVQVSTLQSTFALLVQ 172
 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 DB 98 EESNTIMIMIKINP-HVQGHIMSPHGLINKP-PKPKLQVQVSVQVQV 152
 QY 233 QANNTPTNVVWNNYMKCTAQDQPIFYSNVFHSINCHQVQPKKIDTHTQGVK 202
 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 DB 153 KKKKKSKP-----GQVSK----- 166

RESULT 15

QYXSF3 PRELIMINARY: PRT: 190 AA.

AC QYXSF3
 DT 01-NOV-1999 (EMBLrel. 12, created)
 DT 01-NOV-1999 (EMBLrel. 12, last sequence update)
 DT 01-JUN-2001 (EMBLrel. 17, last annotation update)
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR 164.
 GN VEGF.
 OS Carotis familiaris (dog).
 OC Eukaryota; Metazoa; Chordata; Graculata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID:9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE:HEART;
 RA Submitted by: Roque R.S.;
 RA Submitted (MAR 1993) to the EMBL/Genbank/Genpep databases.
 DR EMBL: AF133248; AAC29682.1; -
 DR HSSP: P15692; 2VPE.
 DR InterPro: IPR000072; PDGF.
 DR Pfam: PF00841; PDGF_1.
 DR ProDom: PD001629; PDGF_1.
 DR SMART: SM00141; PDGF_1.
 DR PROSITE: PS00249; PDGF_1; 1.
 DR PROSITE: PS02784; PDGF_2; 1.
 SV SEQUENCE 190 AA: 22592 MW: 20545 MW: 20545 MW: 20545 MW: CQ664;

Query Match 9.28; Score 214.5; DB 6; Length 190;
 Best Local Similarity 24.88; Pred. No. 1.4e-12;
 Matches 59; Conservative 26; Mismatches 59; Indels 95; Gaps 8;
 QY 109 HYNTEIKSTINWPKTQMPPEVTVVPPVATNTHTKPPVSVYPPNENSTAGMNT 168
 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 DB 84 EVKPKK VVQSVVHPLHPLVQPEVPPPEVPPSGVPI MPQDQCNDELEVPI 97
 QY 169 GNTSTYSLSTLFEITVPL SQPKVITSTFANHTSCGMSTLTVYRQVSHLR 223
 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 DB 93 CVPIEE-----FNITQIDIRKIPDQOHGKSTFQHSKTEGPKKIPAPQ----- 138
 QY 224 SLVATLQVQANAKICTNVVWNNYMKCTAQDQPIFYSNVFHSINCHQVQPKKIDTHTQGVK 202
 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 DB 153 KKKKKSKP-----GQVSK----- 166

Query Match 9.48; Score 217.5; DB 6; Length 214;
 Best Local Similarity 26.48; Pred. No. H.1e-13;
 Matches 62; Conservative 26; Mismatches 75; Indels 79; Gaps 8;
 QY 109 HYNTEIKSTINWPKTQMPPEVTVVPPVATNTHTKPPVSVYPPNENSTAGMNT 168
 111 111 111 111 111 111 111 111 111 111 111 111 111 111

Query Match 9.28; Score 214.5; DB 6; Length 190;
 Best Local Similarity 24.88; Pred. No. 1.4e-12;
 Matches 59; Conservative 26; Mismatches 59; Indels 95; Gaps 8;
 QY 109 HYNTEIKSTINWPKTQMPPEVTVVPPVATNTHTKPPVSVYPPNENSTAGMNT 168
 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 DB 84 EVKPKK VVQSVVHPLHPLVQPEVPPPEVPPSGVPI MPQDQCNDELEVPI 97
 QY 169 GNTSTYSLSTLFEITVPL SQPKVITSTFANHTSCGMSTLTVYRQVSHLR 223
 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 DB 93 CVPIEE-----FNITQIDIRKIPDQOHGKSTFQHSKTEGPKKIPAPQ----- 138
 QY 224 SLVATLQVQANAKICTNVVWNNYMKCTAQDQPIFYSNVFHSINCHQVQPKKIDTHTQGVK 202
 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 DB 153 KKKKKSKP-----GQVSK----- 166

Search completed: February 20, 2002, 16:27:08
 Job time: 191 sec

Gene version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

us protein - protein search, using sw model

Run on: February 20, 2002, 16:24:42 ; Search time 17.06 seconds

(without alignments)
891,905 Million cell updates/sec

Title: us-09-534-376a-11

Sequence: 1 MHLDFELSLACSLAALIP.....SPSEVCGVSTYKKRPHLN 415

Scoring table:

BLDSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 100059 seqs, 4664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_39*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	FR	ID	Description
1	2433	100.0	415	1	VEGC_MOUSE	P97953 mus musculus
2	2048	87.8	412	1	VEGC_HUMAN	F49767 homo sapien
3	271.5	11.6	1700	1	HAR3_CHITE	Q03376 chironomus
4	213.5	9.2	215	1	VEGE_HUMAN	F15592 homo sapien
5	211.5	9.1	190	1	VEGE_PIG	P49151 sus scrofa
6	201.5	8.6	193	1	VEGE_RAT	P16512 ratnus norv
7	198.5	8.5	190	1	VEGE_HUMAN	P15641 bos taurus
8	195.5	8.4	164	1	VEGE_CAVPO	P26617 cavia porce
9	195.5	8.2	214	1	VEGE_MOUSE	Q00741 mus musculu
10	190.5	8.2	473	1	FP2_MYTA	Q25164 mytilus gal
11	179.5	7.7	188	1	VEGC_MOUSE	P49766 mus musculu
12	174.5	7.7	188	1	VEGC_HUMAN	P49765 homo sapien
13	173.5	7.4	146	1	VEGC_SHEEP	P50412 ovis aries
14	173	7.4	216	1	VEGC_CHICK	P52382 galus gall
15	163	7.0	2703	1	NOT2_DROME	F52384 ort vitus (
16	162.5	6.9	143	1	VEGC_DROME	F52384 ort vitus (
17	161.5	6.9	1964	1	MTG4_MOUSE	P07207 drosophila
18	160	6.9	148	1	VEGC_HUMAN	P52385 ort vitus (
19	159.5	6.8	4635	1	VEGC_DROME	P52385 ort vitus (
20	155.5	6.7	2482	1	WME_PIG	Q41901 mus musculu
21	155	6.6	2444	1	WME_HUMAN	Q20833 sus scrofa
22	152.5	6.5	170	1	PLGE_HUMAN	F49543 homo sapien
23	151.5	6.5	2437	1	NOT2_HUMAN	P49763 homo sapien
24	151.5	6.5	2871	1	FRN1_HUMAN	P45555 bos taurus
25	151	6.5	3672	1	EML2_CANF1	Q21313 canorabadi
26	149	6.4	1557	1	EML1_CANF1	Q18823 canorabadi
27	148	6.3	2139	1	GRB_DROME	P10040 drosophila
28	148	6.3	2813	1	WVF_CANF1	Q28265 canis fami
29	147.5	6.3	2521	1	NOT2_XENLA	P21783 xenopus lae
30	147.5	6.3	2531	1	MTG1_MOUSE	Q01705 mus musculu
31	147.5	6.3	2871	1	FRN1_BOVIN	P04133 bos taurus
32	147	6.3	2871	1	FRN1_PIG	P04133 bos taurus
33	146.5	6.3	1790	1	FRN1_DROME	P04133 bos taurus

34	146	6.3	2871	1	FRN1_MOUSE	Q61554 mus musculu
35	145.5	6.2	798	1	TRB1_XENLA	P12606 xenopus lae
36	145.5	6.2	1429	1	L112_CANF1	P14585 canorabadi
37	145.5	6.2	2907	1	FRN2_MOUSE	Q61555 mus musculu
38	145.5	6.2	2911	1	FRN2_HUMAN	P45555 mus musculu
39	145	6.2	1680	1	FRN2_DROME	P40432 drosophila
40	144.5	6.2	1064	1	FRP1_STRPO	P10079 stronyloce
41	144	6.2	798	1	TRB1_HUMAN	P03556 homo sapien
42	142.5	6.1	1746	1	TRN1_PIG	Q29116 sus scrofa
43	142.5	6.1	2541	1	NTG1_RAT	Q07008 rattus norv
44	141	6.0	1808	1	TEN1_CHICK	P10039 galus gall
45	141	6.0	2813	1	WVF_HUMAN	P04275 homo sapien

ALIGNMENTS

RESULT 1
VEGC_MOUSE
ID VEGC_MOUSE STANDARD PRT: 415 AA.
AC P97953;
DE 15-JUL-1998 (Ref. 36, Created)
DE 15-JUL-1998 (Ref. 36, last sequence update)
DE 20-AUG-2001 (Ref. 40, last annotation update)
DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (FL14 LIGAND)
DE (FL14-L).
CN VEGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE=97164697; PubMed=9012504;
RA Kulk E., Lyukavetsaki A., Taira S., Kallipetian A., Jellisch M.,
RT Joukov V., Allitalo K.;
RT *VEGF-C receptor binding and pattern of expression with VEGFR-3
RT suggests a role in lymphatic vascular development.*
RL Development 122:3825-3837(1996).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN-BALB/C;
RC MEDLINE=97388492; PubMed 924716;
RX Fitz L.J., Morris I.C., Towler P., Long A., Burgess P., Genco R.,
RA Wang L., Gassaway K., Nickbarg E., Kovacic S., Gaglietta A.,
RA Gnanapavan J., Timmerly H., Zollner P., Heller P., Lee L.V.,
RA Turner K.L., Wood C.R.;
RA Characterization of murine Flt4 ligand/VEGF-C.*
RL Oncogene 15:613-618(1997).
CC -1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHelial
CELL GROWTH.
CC -1- SIMILARITY: HOMOLOGY: DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC This SwissProt entry is copyright. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See <http://www.isb-sib.ch>)
CC or send an email to license@isb-sib.ch.
DR EMBL: 973620; AAC62984.1; -;
DR EMBL: 058122; AAC66707.1; -;
DR HSSP: P15692; VPF.
DR MSD: MG1:109124; VEGFC.
DR InterPro: IPR002409; EF_Cysknut.
DR InterPro: IPR000072; PDGF.
DR Pfam: PF00841; PDGF_1
DR PRINTS: PR00438; GVEYSKNUT.
DR ProDom: PD001620; PDGF_1.
DR SMART: SM00141; PDGF_1.

1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR PERMEABILITY.

2- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.

3- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY SIMILARITY). BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.

4- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.

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DR EMBL: M64240; AAA37057.1; -

DR HSSP: P15692; 2VCH.

DR InterPro: IPR000972; PDGF

DR Pfam: PF00341; PDGF_1.

DR ProDom: PD001629; PDGF_1.

DR SMART: SM00141; PDGF_1.

DR PROSITE: PS00249; PDGF_1; 1.

DR PROSITE: PS00278; PDGF_2; 1.

DR Mitogen: growth factor: Glycoprotein.

KW Mitogen: growth factor: Glycoprotein.

FT DISULFID 25 67 BY SIMILARITY.

FT DISULFID 56 161 BY SIMILARITY.

FT DISULFID 60 103 BY SIMILARITY.

FT DISULFID 50 50 INTERCHAIN (BY SIMILARITY).

FT DISULFID 59 59 INTERCHAIN (BY SIMILARITY).

FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 164 AA; 19330 MW; 9EBB6A81A9D5DC44 CRC64;

Query Match 8.48; Score 196.5; Pr. 1; Length 164;

Best Local Similarity 22.5%; Pred No. 576-09;

Matches 58; Conservative 28; Mismatches 59; Indels 113; Gaps 9.

QY 89 GMDPPLTFTGDSVFAFAHNTLILKSIDNEMKTCQMPREVCIDVKGKFGAATFF 148

DB 6 GRÖKR-----EVKKY-----DVYKSYRPTLMDVDFQYDPELEYIF 46

QY 149 KPPVSVYRGCCNSGLCCNNTGYSLTFLFTVL-----SGPKVTLISFANHT 203

DB 47 KESYVPLMPVCCCNCFSTFVPLPE-----FNTLMIMIKRQGHIGSESLGHS 99

QY 204 SGCKMSKIDYKOVHSLIRSLATILPQCVANKICPTNVMNRMGSLAQGNPIFYSN 263

DB 100 KETLKKKKKKK----- 112

QY 264 VELDSTNGHVGGRKLEETGQVCKPTKPSGCKPKEL--PDSGQVCKNFI 320

DB 113 -----ENPCGCS-----KKHLFVDQDTGCGSCNN-- 141

QY 421 PNSCGANR-EPDENTGQC 437

DB 142 ESKGKAHOLELHETPFG 159

RESULT 9

VEGF_MOUSE STANDARD: PRY 214 AA.

AP 000731:

DI 01-APR-1993 (Ref. 25, created)

DI 01-OCT-1996 (Ref. 34, last sequence update)

DI 20-AUG-2001 (Ref. 40, last annotation update)

DI VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VPGF) (VASCULAR

DI HERMABILITY FACTOR) (VEGF).

DI VEGF.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090:

RN [1]

RA SEQUENCE FROM N.A. PubMed:1592003;

RA BREIER G., Albrecht U., Sterrer S., Kisan M.;

RT "Expression of vascular endothelial growth factor during embryonic angiogenesis and endothelial cell differentiation.";

RL Development 114:521-532(1992).

RN [2]

RP SEQUENCE FROM N.A. (VEGF-1).

RP MEDLINE:92355593; PubMed:1644816;

RA Claffey R.P., Mjackson W.O., Spiegelman B.M.;

RT "Vascular endothelial growth factor. Regulation by cell differentiation and activated second messenger pathways.";

RL J. Biol. Chem. 267:16317-16322(1992).

RN [3]

RP SEQUENCE OF 1-3 FROM N.A.

RA MEDLINE:96216498; PubMed:8632007;

RA Shima D.T., Kuroki M., Deutsch U., Ng Y., Adams A.P., D'Amore P.A.;

RT "The mouse gene for vascular endothelial growth factor. Genomic structure, definition of the transcriptional unit, and characterization of transcriptional and post-transcriptional regulatory sequences.";

RL J. Biol. Chem. 271:3877-3884(1996).

CC 1- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR PERMEABILITY.

CC 1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.

CC 1- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.

CC 1- ALTERNATIVE PRODUCTS: THREE FORMS (VEGF-1, VEGF-2 AND VEGF-3) ARE PRODUCED AS A RESULT OF ALTERNATIVE SPLICING OF THE SAME GENE. THE LONGEST FORM (VEGF-3, SHOWN HERE) CONTAINS A BASIC INSERT LINKED TO CELL-ASSOCIATION/HEPARIN-BINDING.

CC 1- TISSUE SPECIFICITY: IN DEVELOPING EMBRYOS, EXPRESSED MAINLY IN THE CHOROID PLEXUS, PARAVENTRICULAR NEUROEPITHELIUM, PLACENTA AND KIDNEY GLomeruli. ALSO FOUND IN BRONCHIAL EPITHELIUM, ADRENAL GLAND AND IN SEMINIFEROUS TUBULES OF TESTIS. HIGH EXPRESSION OF VEGF CONTINUES IN KIDNEY GLOMERULI AND CHOROID PLEXUS IN ADULTS.

CC 1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.

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CC EMBL: S37052; AB02252.1; -

CC EMBL: S38083; AB02253.1; -

CC EMBL: S44109; AB02254.1; -

CC EMBL: M95200; AAA40547.1; -

CC EMBL: U41863; -; NOT_ANNOTATED_CDS.

CC PIR: A43351; A43351.

CC HSSP: P15692; 2VCH.

CC MGD: MG1:103178; VEGF.

CC InterPro: IPR000972; PDGF.

CC Pfam: PF00341; PDGF_1.

CC ProDom: PD001629; PDGF_1.

CC SMART: SM00141; PDGF_1.

CC PROSITE: PS00249; PDGF_1; 1.

CC PROSITE: PS00278; PDGF_2; 1.

CC Mitogen: growth factor: Glycoprotein; Alternative splicing: Signal.

KW Mitogen: growth factor: Glycoprotein.

FT SIGNAL 1 26

FT CHAIN 27 214

FT DISULFID 51 93 BY SIMILARITY.

FT DISULFID 82 127 BY SIMILARITY.

FT DISULFID 86 129 BY SIMILARITY.

FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).

FT DISULFID 85 85 INTERCHAIN (BY SIMILARITY).

FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (PROBABLE).


```

07 164 NSBGLQWNTSLFSLFLVPLVSG-----GKRVL-----LSFANHLCKMMSKL 211
08 165 KNSBGLQWNTSLFSLFLVPLVSG-----GKRVL-----LSFANHLCKMMSKL 211
09 166 KNSBGLQWNTSLFSLFLVPLVSG-----GKRVL-----LSFANHLCKMMSKL 211
10 212 IVYVAVHSTLPPSLPATL-----AANRTPTRVYVNN-----WCPPLAAWCTIFYS 262
11 221 -----PGRPPPRFRVYVAPPPKMAHSSSSSSSSSSSSSSSSSSSSSSSSSSSS 256
12 263 NVEHDSINRTH -----PAMNKNKLDEDT-----QVCGKGLRPSNG ----- 301
13 267 KAGSGLTAVVAVKLTCKNSSSKLVHNGSYNCKGGSGLGLNCKNKP 310
14 402 -----PKRLEDSRQV-----SNLFTNSANPFRNTQVVFSTCPN 346
15 411 QGNRQVVPNSIDAFKRVVAVKRPCTK-----PNN-----NINCKKMSKCNVN 360
16 447 QPLNKGKAV-----ETEE-----NTCKFLKGRKF-----HIOT 376
17 461 QKTTKAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 420
18 377 GSCYR-----RPGANRKHDPGLSPSEVCGVPSY 408
19 421 KSKYKKNHCAAPKPKNPKTKDKKNY-----VCKVAPRY 456
20
21 RESULT 11
22 VEGF_MOUSE STANDARD PRT 188 AA.
23
24 01-OCT-1996 (Rel. 34, Created)
25 01-OCT-1996 (Rel. 34, Last sequence update)
26 20-AUG-2001 (Rel. 40, Last annotation update)
27 VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VASCULAR
28 ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRF).
29 VEGF OR VRF.
30 Mus musculus (Mouse).
31 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
32 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
33 NCBI_taxonomy:10090.
34
35 SEQUENCE FROM N.A.
36
37 MEDLINE-9618755; PubMed-8637916;
38 MEDLINE-9618755; PubMed-8637916;
39 Johnson B., Palusela K., Kalpajna A., von Euler G., Jonkov V.,
40 Saksela E., Orpana A., Pettersson R. F., Alitalo K., Eriksson U.;
41 "Vascular endothelial growth factor B, a novel growth factor for
42 endothelial cells."
43 Proc. Natl. Acad. Sci. U.S.A. 94:2576-2581(1996).
44
45 SEQUENCE FROM N.A.
46
47 MEDLINE-9618755; PubMed-8607868;
48 Johnson S., Latoranz J., Grimond S., Silins G.,
49 Nordensjoeld M., Weber G., Hayward N.K.;
50 "Characterization of the murine VEGF-related factor gene."
51 Biochem. Biophys. Res. Commun. 220:922-928(1996).
52
53 FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
54
55 SHUNT: HOMODIMER. DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER
56 WITH VEGF.
57
58 SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
59 TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN. KIDNEY
60 AND SKELETAL MUSCLE.
61
62 SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS
63
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70 or send an email to license@isb.slb.ch).

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07 164 NSBGLQWNTSLFSLFLVPLVSG-----GKRVL-----LSFANHLCKMMSKL 211
08 165 KNSBGLQWNTSLFSLFLVPLVSG-----GKRVL-----LSFANHLCKMMSKL 211
09 166 KNSBGLQWNTSLFSLFLVPLVSG-----GKRVL-----LSFANHLCKMMSKL 211
10 212 IVYVAVHSTLPPSLPATL-----AANRTPTRVYVNN-----WCPPLAAWCTIFYS 262
11 221 -----PGRPPPRFRVYVAPPPKMAHSSSSSSSSSSSSSSSSSSSSSSSSSSSS 256
12 263 NVEHDSINRTH -----PAMNKNKLDEDT-----QVCGKGLRPSNG ----- 301
13 267 KAGSGLTAVVAVKLTCKNSSSKLVHNGSYNCKGGSGLGLNCKNKP 310
14 402 -----PKRLEDSRQV-----SNLFTNSANPFRNTQVVFSTCPN 346
15 411 QGNRQVVPNSIDAFKRVVAVKRPCTK-----PNN-----NINCKKMSKCNVN 360
16 447 QPLNKGKAV-----ETEE-----NTCKFLKGRKF-----HIOT 376
17 461 QKTTKAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 420
18 377 GSCYR-----RPGANRKHDPGLSPSEVCGVPSY 408
19 421 KSKYKKNHCAAPKPKNPKTKDKKNY-----VCKVAPRY 456
20
21 RESULT 12
22 VEGF_HUMAN STANDARD PRT 188 AA.
23
24 01-OCT-1996 (Rel. 34, Created)
25 01-OCT-1996 (Rel. 34, Last sequence update)
26 20-AUG-2001 (Rel. 40, Last annotation update)
27 VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED
28 FACTOR).
29 VEGF OR VRF.
30 Homo sapiens (human).
31 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
32 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
33 NCBI_taxonomy:9606.
34
35 SEQUENCE FROM N.A.
36
37 MEDLINE-9618755; PubMed-8637916;
38 MEDLINE-9618755; PubMed-8637916;
39 Johnson B., Palusela K., Kalpajna A., von Euler G., Jonkov V.,
40 Saksela E., Orpana A., Pettersson R. F., Alitalo K., Eriksson U.;
41 "Vascular endothelial growth factor B, a novel growth factor for
42 endothelial cells."
43 Proc. Natl. Acad. Sci. U.S.A. 94:2576-2581(1996).
44
45 SEQUENCE FROM N.A.
46
47 MEDLINE-9618755; PubMed-8607868;
48 Johnson S., Latoranz J., Grimond S., Silins G., Johnson S.,
49 Nordensjoeld M., Weber G., Hayward N.K.;
50 "Cloning and characterization of a novel human gene related to
51 vascular endothelial growth factor."
52 Genome Res. 6:124-131(1996).
53
54 FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.
55
56 SHUNT: HOMODIMER. DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER
57 WITH VEGF.
58
59 SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR
60 TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN. KIDNEY
61 AND SKELETAL MUSCLE.
62
63 SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS
64
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71 or send an email to license@isb.slb.ch).

```

TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.

1. TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXCEPT LIVER.

2. HIGHEST LEVELS FOUND IN HEART, SKELETAL MUSCLE AND PANCREAS.

3. SIMILARITY: BELONGS TO THE PRO-VEGF FAMILY OF GROWTH FACTORS.

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EMBL: BAB001; AAB062/4.1; -

EMBL: U3405; AAO7463.1; -

EMBL: P15692; VPE; -

EMBL: A01508; -

InterPro: IP000072; PROGF; -

ProDom: P000441; PROGF; 1; -

ProDom: P000429; PROGF; 1; -

SMART: SM00141; PROGF; 1; -

ProSITE: PS00249; PROGF; 1; -

ProSITE: PS0278; PROGF; 2; 1; -

ProSITE: PS0278; PROGF; 2; 1; -

Metagen: Growth factor: Signal: Heparin binding.

FT SIGNAL: 1 21

FT CHAIN: 22 188

SEQUENCE: 188 AA; 21461 MW; P0464DFA3727104 CRC64;

Query Match: 7.7%; Score 178.5; DB 1; Length 188;

Best Local Similarity: 27.5%; Pred. No. 1; No. 07;

Matches: 42; Conservative: 24; Mismatches: 75; Indels: 49; Gaps: 7;

UY 107 AAMHMLKLSLNNKMBLQFMRVLDWKEEGCAALINLEKRVSVYVGGSSNSAG 106

DB 28 ADEHGKRVKSLDLYTKATLPQREVYVPLVLELMGTYAKQIVSGYVQKGGCCGDDG 86

UY 167 LQVNTSTVYLSKTLPELTVLSQCKPVITSPANHTSGKMSKIDVYGVHSLIKRSLP 226

DB 67 LEVVTGQHVQMOILMKRYSSQAF---MSIPEHSQETPRK---KKSAVAKDPS 148

UY 227 AELIQVQAN-----KQPIINYVNNVNCQPLAGQCFPSVNEHDSINQIHVGSPNK 280

DB 139 KDLTKRGLQHQKQKPKR-----KGRG-----KRSPLQCGVPR 174

UY 281 ELLEPTQV 289

DB 175 ELNPTQV 183

RESULT 14

VEGF_SHEEP STANDARD: PROT: 146 AA.

AC P50412;

DT 01-OCT-1996 (Ref. 44, Cited)

DT 01-OCT-1996 (Ref. 44, Last sequence update)

DT 20-MAY-2001 (Ref. 40, Last annotation update)

DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPE).

OS VEGF.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Eularchia; Euarchantaria; Primates; Haplorhina; Carnivora; Artiodactyla; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Caprinae; Capri; -

OX NCBI_TaxID=9041; 93944;

KN 111

RP SEQUENCE FROM N.A.

RC TISSUE: Kidney;

RC MEDLINE 9/11/98; PubMed 8758842;

RA Bredem D.A., Dai Y., Li J., Blalock Jones D.S., Smith S.K., Reynolds L.P., Mori R.M.;

RA Neuroendocrine and expression of vascular endothelial growth factor (VEGF) in the ovine corpus luteum.;

PL 3. Referred. P0111; 108;157;165(1996).

CC 1. FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR PERMEABILITY.

CC 2. SUBONITE: HOMODIMER, DISULFIDE-LINKED.

CC 3. SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY SIMILARITY).

CC 4. SIMILARITY: BELONGS TO THE PRO-VEGF FAMILY OF GROWTH FACTORS.

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EMBL: X89506; CAA61677.1; -

EMBL: P15692; VPE; -

EMBL: P15692; VPE; -

InterPro: IP000072; PROGF; -

ProDom: P000441; PROGF; 1; -

ProDom: P000429; PROGF; 1; -

SMART: SM00141; PROGF; 1; -

ProSITE: PS00249; PROGF; 1; -

ProSITE: PS0278; PROGF; 2; 1; -

Metagen: Growth factor: Glycoprotein: Signal:

FT SIGNAL: 1 26

FT CHAIN: 27 146

FT DISULFID: 51 93

FT DISULFID: 82 127

FT DISULFID: 86 129

FT DISULFID: 76 76

FT DISULFID: 85 85

FT CARGLYCD: 100 100

SEQUENCE: 146 AA; 17247 MW; 4F792CB5791760 CRC64;

Query Match: 7.4%; Score 173.5; DB 1; Length 146;

Best Local Similarity: 33.9%; Pred. No. 4; No. 07;

Matches: 37; Conservative: 17; Mismatches: 42; Indels: 14; Gaps: 3;

UY 113 ELKSLDNNKRTQMPVEVLDWKEEGCAALINLEKRVSVYVGGSSNSAG 172

DB 38 EVMKRPD-VQHSFGRPLELVDLQEVDFLETFEFSVPLMKGGKNDSELRVPT 96

UY 173 SLGYLSKTLPELTVLSQCKPVITSPANHTSGKMSKIDVYGVHSLIKRSLP 216

DB 97 EEL-----FNTMQIMKIPQSHIGEMSPDQHNCRGTRKQKARQ 138

RESULT 14

VEGF_CHICK STANDARD: PROT: 216 AA.

AC P52582; Q91420;

DT 01-OCT-1996 (Ref. 34, Cited)

DT 15-JUL-1998 (Ref. 36, Last sequence update)

DT 20-MAY-2001 (Ref. 40, Last annotation update)

DE VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPE).

OS VEGF.

OS Gallus gallus (Chicken); and

OS Coturnix coturnix japonica (Japanese quail).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neornithae; Galliformes; Phasianidae; Phasianinae; Gallus; -

OX NCBI_TaxID=9041; 93944;

KN 111

RP SEQUENCE FROM N.A.

RC SPECTROPHOTOKIN TISSUE: Heart;

RC Takahashi T.;

RA Submitted (FBI-1998) to the EMBL/Genbank/DDBJ databases. [2]


```

25 81 YKQJLRKRWKQPLINTFTRSVKFAAHY-----NTEILKSIDNEN 122
   | | | | | | | | | | | | | | | | | | | | | | | |
10 356 YSC-ICVNMWAGLDCSNNI-UDKQACFYCAT-IDGVGSFYCQJLKKJDLCHLDAC 413
   | | | | | | | | | | | | | | | | | | | | | | | |
07 128 FETGMPPEVY-IDVJEEZAA-TTFEEFCVA-YYHC--GAGCNSELDGCMNTSTCY 176
   | | | | | | | | | | | | | | | | | | | | | | | |
10 414 TSNCHALATIDTSPINISYASCAIGKIDGNSHDIDFEDGSPFHNNI-CVNIHGSY 472
   | | | | | | | | | | | | | | | | | | | | | | | |
07 177 LSKTIFELIVP-SQSPKIVT-ISPANTSP----CMKILVYRQVHS11RSLJA-TLP 230
   | | | | | | | | | | | | | | | | | | | | | | | |
10 473 KQWFSQSPF-----GPRCEININEFSHPQNEBSCLIDPTEFCV-----CMPGFTCP 521
   | | | | | | | | | | | | | | | | | | | | | | | |
07 241 QCGAANKTTPPNVYNNNMWGLAQDPFIYSNVEDLSTNGFIDV*-----CPNKEIDH 285
   | | | | | | | | | | | | | | | | | | | | | | | |
10 522 QCEIUIIDHOSNPMIINAGTCH-----DKINCFKQSCALDPIGARCOINID 566
   | | | | | | | | | | | | | | | | | | | | | | | |
07 286 TQV-----QVKKSLRPSQ-----GP-HK-----ELIDRSCQ 312
   | | | | | | | | | | | | | | | | | | | | | | | |
10 567 EYQNGFTRNBI-THSTARYSPFPAYITSTFTININ--TSNCTHCK-TEFVNSFKY 626
   | | | | | | | | | | | | | | | | | | | | | | | |
07 313 C-----VCKNKLPPNSQANR-EPDENTQ-----CVCK-----RTPYNN----- 346
   | | | | | | | | | | | | | | | | | | | | | | | |
10 627 QDPAYTYICQKI--NEFESNPQFDSH-QQHVBSYVQVAGTSGKMEVNVNECHS 683
   | | | | | | | | | | | | | | | | | | | | | | | |
07 447 QFINPG-----KFA*-----ETENTLCKE-----LKKK----- 471
   | | | | | | | | | | | | | | | | | | | | | | | |
10 684 NPONNBAGTTHATNSYKQGVVSE113JHCKKNVHCTSSPCANNGVTHVANDYKQPCPY 743
   | | | | | | | | | | | | | | | | | | | | | | | |
07 472 -FHHQTC-----SCYRPPCANRLEKHTDGLSFESEV-RCVPSY 408
   | | | | | | | | | | | | | | | | | | | | | | | |
10 744 GPYIAHCTLSQVRCASNPQVNF-QRCDEGT--NEFFICHPGKY 783

```

Search completed: February 20, 2002, 16:27:42
Job time: 170 sec



Genome version 4.5
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3M protein - protein search, using SW model

Run on: February 20, 2002, 16:20:52, Search time 27.95 seconds

(without alignments)
1222 978 Million cell updates/sec

Title: us-09-534-376a-11

Percent score: 43.33

Sequence: 1 MHLGFLSLAGSLAALIP.....SFSEVRCVSTWKPPLN 415

Scoring table:

Gapop 10.0, Gapext 0.5

Starched: 219241 seqs, 76174562 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Database: 1: PIR-68:*

2: PIR1:*

3: PIR2:*

4: PIR4:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	2048	87.8	419	2 S69207
2	271.5	11.6	1797	2 S68167
3	241	9.9	232	2 A41751
4	211.5	9.1	190	2 S52130
5	201.5	8.6	190	2 A35087
6	200.5	8.6	190	2 B44881
7	198.5	8.5	190	2 B40080
8	195.5	8.4	214	2 A41981
9	190.5	8.2	473	2 A56175
10	181	7.8	160	2 J60542
11	179.5	7.7	188	2 J63480
12	176.5	7.6	232	2 T02091
13	173.5	7.4	146	2 S57956
14	172.5	7.4	139	2 A33787
15	170	7.3	247	2 A41128
16	167	7.2	1204	2 A43175
17	164	7.0	2704	2 A24420
18	161.5	6.9	1964	2 T09059
19	160	6.9	148	2 D49530
20	159.5	6.8	144	2 B49520
21	159.5	6.8	3645	2 T10053
22	157	6.7	1372	2 T25933
23	154.5	6.6	149	2 A41236
24	151.5	6.6	2555	2 A40843
25	151.5	6.5	2432	2 S42632
26	151.5	6.5	4882	2 A47231
27	151	6.5	3672	2 T23433
28	151	6.5	3704	2 T37416
29	149.5	6.4	545	2 T14108

ALIGNMENTS

RESULT 1
S69207
Vascular endothelial growth factor C precursor - human
M:Alternate names: FLT4 ligand bHM
C:Species: Homo sapiens (man)
C:Date: 27-Apr-1996 #sequence, revision 01-Nov-1996 #text, change 08-Oct-1999
C:Accession: S69207, #sequence, S71443; S69208; 072659
R:Joukov, V.; Pajusola, K.; Kaipainen, A.; Chlilov, D.; Lahninen, I.; Kukk, E.; Saksela
EMBO J. 15, 1751, 1996
A>Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand
A:Reference number: S69207; MIM:602004
A:Accession: S69207
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-419 <300>
A:Cross references: EMBL:X6216; NID-01172488; PIRN:CAAC3907; PIR:Q221096; PIR:Q118
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, December 1995
A>Note: only a part of the translation is shown
R:Lee, J.; Gray, A.; Yuan, J.; Inoh, S.M.; Avraham, H.; Wood, W.L.
submitted to the EMBL Data Library, December 1995
A:Description: Vascular endothelial growth factor related protein (VRP): A ligand and
A:Reference number: S69208
A:Accession: S69208
A:Molecule type: mRNA
A:Residues: 1-419 <300>
A:Cross references: EMBL:U41442; NID-01150988; PIRN:AAAB214.1; PIR:Q1150989
R:Morris, J.C.
submitted to the EMBL Data Library, May 1996
A:Reference number: H01557
A:Accession: 002659
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-419 <300>
A:Cross references: EMBL:U56111; NID-01373426; PIRN:AAH02997.1; PIR:Q1374427
C:Genes:
A:Gene: VEGFC, VRP
A:Cross references: GDB:3890883; OMIM:601528
F1 (2/Domain) Signal sequence #status predicted -SIG-
F1 (1/2/Domain) FGF-like #status predicted -PRO-

[illegible][illegible]



KM Human: receptor tyrosine kinase; RTK; Flt4; fms like tyrosine kinase 4;
 KM VEGFR-C: vascular endothelial growth factor receptor-3; chromosome 3q35;
 KW cytotlastic tumour imaging; anti-tumour therapy; treatment; diagnosis;
 KW neoplastic diseases; lymphoma; carcinoma; breast; squamous cell; melanoma;
 KW sarcoma; malignancy; VEGF-C; vascular endothelial growth factor C;
 XX
 OS Homo sapiens.
 FH
 FH Key location/qualifiers
 FH Peptide 1..31
 FH /label= Signal peptide
 FT 32..103
 FT /label= N-terminal peptide
 FT /note= "cleavage of this peptide from partially processed
 VEGF-C produces a fully processed mature form of VEGF-C
 of 21-23 kD which has high affinity to VEGFR-2"
 FT 104..227
 FT /label= Mature_VEGF-C
 FT Peptide 228..419
 FT /label= C-terminal peptide
 FT /note= "this protein is a product of a specific testis
 remnant of a Balb/c rat 3 protein (BR3P) sequence;
 cleavage of signal peptide and the C-terminal
 peptide produces a partially processed form of VEGF-C of
 about 29 kD which has high affinity to Flt4 (VEGFR-3)"
 FT Binding-site 131..211
 FT /note= "The 131-211 amino acid region of VEGFR-3 is
 at position 156 is essential for VEGFR-2 binding and at
 165 is essential for VEGFR-2 and VEGFR-3 binding"
 FT Region 131..211
 FT /note= "Important for VEGF-C activity"
 XX W:200021550-A1.
 XX 20-Apr-2000.
 XX 08-OCT-1999; 99WO-0523525.
 XX 09-OCT-1998; 98US-0169074.
 XX (LUDWIG) INST CANCER RES.
 XX (OYME-) UNIV HELSINKI LICENSING LTD OY.
 XX
 PI Alitalo K, Kaipainen A, Valtola R, Jussila J.
 XX W61: 2000-317656/27.
 XX
 XX Treating neoplastic diseases such as lymphoma, carcinoma, melanomas
 PI and sarcomas, involves administering a compound capable of inhibiting
 PI binding of ligand proteins to fms like tyrosine kinase 4 receptor -
 XX
 PS Example 15-17, page 140-142; 14pp; English.
 XX
 XX The patent discloses a method to treat neoplastic disease characterised
 XX by expression of fms like tyrosine kinase 4 (Flt4) receptor (also
 XX referred as vascular endothelial growth factor receptor-3, VEGFR-3) in
 XX endothelial cells of blood vessels adjacent to malignant neoplasm. The
 XX method involves administering a compound that inhibits binding of a
 XX ligand to Flt4 thereby inhibiting Flt4 mediated proliferation of vascular
 XX endothelial cells. The compound is useful for treating neoplastic disease
 XX such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas
 XX and sarcomas. Flt4 receptor tyrosine kinase binding compounds can be used
 XX for manufacturing medicine useful for diagnostic screening, imaging and
 XX treatment of malignancies characterised by Flt4-expressing blood cells
 XX The Flt4 gene maps to chromosomal region 3q35 and is expressed as 5.8 kb
 XX and 4.5 kb mRNAs which differ in their 3' sequences and are
 XX differentially expressed in MEL and DAMI cell lines. Flt4
 XX belongs to a subfamily of class III receptor tyrosine kinases (RTKs).
 XX It is used as a target for tumour imaging and anti-tumour therapy.
 XX The present sequence is a human prepro-vascular endothelial growth
 XX factor C (VEGF-C), a specific example of Flt4 binding compound.
 XX
 XX Sequence 419 AA:

Query Match 67 99; Score 2048; PR 21; Length 419;
 best local similarity 85.44; Prod. No. 7,96-151;
 Matches 358; Conservative 28; Mismatches 29; Indels 4; Gaps 1;
 QY 1 MHLDFSLAGSLAAALPSPREPATVAVFESGLSPSEAPPGSGVAKFEKLEFGL 60
 LB 1 MHLDFSLAGSLAAALPSPREPATVAVFESGLSPSEAPPGSGVAKFEKLEFGL 60
 QY 61 PESSVDFPMVAVIPYVWKKWKKQCFKKGWQ----QPTNPTGDSVKAAMNTEFLK 116
 LB 61 PESSVDFPMVAVIPYVWKKWKKQCFKKGWQ----QPTNPTGDSVKAAMNTEFLK 116
 QY 62 PESSVDFPMVAVIPYVWKKWKKQCFKKGWQ----QPTNPTGDSVKAAMNTEFLK 120
 LB 62 PESSVDFPMVAVIPYVWKKWKKQCFKKGWQ----QPTNPTGDSVKAAMNTEFLK 120
 QY 117 STDNFWPKTQMPDPVQIVWSEKPEKSAINTEPKPPVSVVPPQSGQNSPQVKNISTGY 176
 LB 117 STDNFWPKTQMPDPVQIVWSEKPEKSAINTEPKPPVSVVPPQSGQNSPQVKNISTGY 176
 QY 122 SDNWDKLGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPP 180
 LB 122 SDNWDKLGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPP 180
 QY 177 LSKTLEFETVPLNSQPKVITTSFANHTSPKMSKLVYKQVHSLIPRSLPAILPQVAA 216
 LB 177 LSKTLEFETVPLNSQPKVITTSFANHTSPKMSKLVYKQVHSLIPRSLPAILPQVAA 216
 QY 181 LSKTLEFETVPLNSQPKVITTSFANHTSPKMSKLVYKQVHSLIPRSLPAILPQVAA 240
 LB 181 LSKTLEFETVPLNSQPKVITTSFANHTSPKMSKLVYKQVHSLIPRSLPAILPQVAA 240
 QY 237 KCTGTHVW 296
 LB 237 KCTGTHVW 296
 QY 241 KCTGTHVW 300
 LB 241 KCTGTHVW 300
 QY 352 PFTFNTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 416
 LB 352 PFTFNTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 416
 QY 361 PFTFNTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419
 LB 361 PFTFNTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419
 RESULT 10
 AAY70982
 ID AAY70982 standard; Protein: 419 AA.
 AC AAY70982;
 XX
 DT 09-AUG-2000 (first entry)
 XX
 XX Human vascular endothelial growth factor (VEGF)-C protein.
 XX
 XX Vascular endothelial growth factor (VEGF; human; re-endothelialisation;
 KW vascular endothelial growth factor receptor; VEGFR; vascular trauma;
 KW blood vessel; cardiovascular surgery; anti-restenosis agent; prevention;
 KW restenosis; stenosis; percutaneous transluminal coronary angioplasty;
 XX
 OS Homo sapiens.
 FH
 FH Key location/qualifiers
 FH Peptide 1..31
 FH /label= Signal peptide
 FT 32..103
 FT /note= "cleavage results in partially processed VEGF-C
 protein (29 kD)"
 FT 104..227
 FT /label= Mature_VEGF-C
 FT /note= "Processed vascular endothelial growth factor-C"
 FT Binding-site 131..211
 FT /note= "Essential for VEGFR-2 and VEGFR-3 binding"
 FT Active-site 131..211
 FT /note= "Essential for biological activity of protein"
 FT Binding-site 137
 FT /note= "Essential for VEGFR-2 and VEGFR-3 binding"
 FT Binding-site 156
 FT /note= "Essential for VEGFR-2 binding"
 FT Binding-site 165

